

**AMENDMENTS TO THE SPECIFICATION:**

In compliance with 37 C.F.R. § 1.823(a), please insert the attached substitute paper copy of the Sequence Listing after the last page of the above-identified application in place of the Sequence Listing previously filed on December 12, 2003.

Please replace paragraph **[0030]** with the following amended paragraph:

**[0030]** Figure 1. ClustalW alignment of proteins GhKOR (SEQ ID No 6), and LeCel3 (Accession number T07612; SEQ ID No 24) and AtKOR1 (Accession number At5g49720; SEQ ID No 5) and BnCel16 (Accession number CAB51903; SEQ ID No 25). Features highlighted are: polarized targeting motifs implicated in targeting to the cell plate (Zuo et al., 2000); a putative transmembrane region near the N-terminus (transmembrane); four of the conserved residues potentially involved in catalysis (Asp-198, Asp-201, His-516 and E-555; labeled o) and representing part of the strong similarity to family 9 glycoside hydrolases; a C-terminal region rich in Pro and characteristic of membrane-bound members of the endo-1,4- $\beta$ -glucanase family; 8 putative N-glycosylation sites (Asn-X-Ser/Thr; labelled G1 to G8).

Please replace paragraph **[0033]** with the following amended paragraph:

**[0033]** Figure 4. Alignment of the Aglu-3/RSW3 sequence (Genbank NP\_201189; SEQ ID NO 26) with the sequences of ER-resident glucosidase II enzymes from potato (Accession number T07391; SEQ ID NO 27), mouse (NP\_032086; SEQ ID NO 28) and fission yeast (CAB65603; SEQ ID NO 29). The clade 2 of Monroe *et al.*

(1999) are shown to demonstrate the high conservation. They include several residues implicated in catalysis (Asp 512 and Asp 617; \*). The site of the *rsw3-1* mutation (Ser599●) is close to these consensus sequences and is conserved in these and other glucosidase II sequences. Predicted N-terminal signal sequences are boxed. No HDEL ER-retention sequences occur at the C-terminus.

Please replace paragraph **[0034]** with the following amended paragraph:

**[0034]** Figure 5. Alignments of the proposed  $\beta$ -subunits of Arabidopsis (At5g56360; SEQ ID NO 30) and rice (our amendment of BAA88186; SEQ ID NO 31) with the  $\beta$ -subunits of glucosidase II from mouse (AAC53183; SEQ ID NO 32) and fission yeast (BAA13906; SEQ ID NO 33). Note the predicted N-terminal signal sequences (boxed), C-terminal H/VDEL ER-retention signals and the mannose-receptor homology region (MHR) near the N-terminus. The 6 cysteines within the MHR (four only in yeast) are numbered and the R and Y residues implicated in substrate-binding (●) and the substrate recognition loop between cysteines 5 and 6 are marked. Elsewhere in the sequence, note the relatively high level of similarity in the N- and C-terminal domains and the much lower similarity and plant-specific inserts in the central region.